PCT/09

ENTERED

Serial Number: 09/8●,000

CRF Processing Date: 5/21/2001
Edited by: _____
Verified by: _____ (STIC staff)

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically:
  _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____.

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically:
  _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
  _____

- [✓] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: 1

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: .

- [ ] Deleted extra, invalid, headings used by an applicant, specifically:
  _____

- [✓] Deleted: [✓] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____.

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically:
  _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically:
  _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [✓] Other: Seqs 38, 58, 148 - deleted nos. under stop codons
  _____
  _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

P

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,000

DATE: 05/21/2001
TIME: 08:37:41

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Output Set: N:\CRF3\05212001\I831000.raw

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PP. 24,32,42

ERRORED SEQUENCES

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,000

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TIME: 08:37:42

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PATENT APPLICATION: US/09/831,000   TIME: 08:37:42

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,000

DATE: 05/21/2001
TIME: 08:37:42

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Output Set: N:\CRF3\05212001\I831000.raw

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PATENT APPLICATION: US/09/831,000   TIME: 08:37:42

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Output Set: N:\CRF3\05212001\I831000.raw

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,000

DATE: 05/21/2001
TIME: 08:37:42

Input Set : A:\53683 seq listing.txt
Output Set: N:\CRF3\05212001\I831000.raw

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Input Set : A:\53683 seq listing.txt
Output Set: N:\CRF3\05212001\I831000.raw

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Input Set : A:\53683 seq listing.txt
Output Set: N:\CRF3\05212001\I831000.raw

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P. 49

RAW SEQUENCE LISTING

DATE: 05/21/2001

PATENT APPLICATION: US/09/831,000

TIME: 08:37:43

Input Set : A:\53683 seq listing.txt
Output Set: N:\CRF3\05212001\I831000.raw

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6051     210                 215                 220
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6079                  325                 330                 335
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6082 Lys Leu Tyr Glu Leu Asn Leu Glu Thr Leu Ser His Ile Ala Glu Ser
6083                  340                 345                 350
6085 cag gtt ttt aac ttg ccg gca aat agc atg tta tcg tta tca gta aat   1104
6086 Gln Val Phe Asn Leu Pro Ala Asn Ser Met Leu Ser Leu Ser Val Asn
6087           355                 360                 365
6089 gat caa gag gtc gta ttt tca atg ttt aaa att gta tat aat aca cct   1152
6090 Asp Gln Glu Val Val Phe Ser Met Phe Lys Ile Val Tyr Asn Thr Pro
6091      370                 375                 380
6093 aag gtt ggt ggt aaa att cta aac gaa att gta tat att act aat tac   1200
6094 Lys Val Gly Gly Lys Ile Leu Asn Glu Ile Val Tyr Ile Thr Asn Tyr
6095 385                 390                 395                 400
6097 atg tac acc aaa tac agt gaa aat tat cag cta acc aac aca ttt agg   1248
6098 Met Tyr Thr Lys Tyr Ser Glu Asn Tyr Gln Leu Thr Asn Thr Phe Arg
6099                  405                 410                 415
6101 cgg aat gta atg aac atg tat gaa gtt tta aca aca att aaa tta aac   1296
6102 Arg Asn Val Met Asn Met Tyr Glu Val Leu Thr Thr Ile Lys Leu Asn
6103           420                 425                 430
6105 gtc aca gat tct tct gtg ttt tat ccg tat ata ttg ttc aca tcc atg   1344
6106 Val Thr Asp Ser Ser Val Phe Tyr Pro Tyr Ile Leu Phe Thr Ser Met
6107           435                 440                 445
6109 tgt aat aat gta gag ata tca tat atg att aat caa ata gca aag ccc   1392
6110 Cys Asn Asn Val Glu Ile Ser Tyr Met Ile Asn Gln Ile Ala Lys Pro
6111      450                 455                 460
6113 gat gac atc acc ata ttt cgc gtg ttt tcg cct tgt ttt tta agc tta   1440
6114 Asp Asp Ile Thr Ile Phe Arg Val Phe Ser Pro Cys Phe Leu Ser Leu
6115 465                 470                 475                 480
6117 agg ttt gat tta gat gaa aac aag cta cga tcc gac gca ccg cag acg   1488
6118 Arg Phe Asp Leu Asp Glu Asn Lys Leu Arg Ser Asp Ala Pro Gln Thr
6119                  485                 490                 495
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6121 tca aaa aga acc ggc tcg gaa ctg gca caa gga gcg tct ggt ttt tgg   1536
6122 Ser Lys Arg Thr Gly Ser Glu Leu Ala Gln Gly Ala Ser Gly Phe Trp
6123             500                 505                 510
6125 cgg ctg ttg cac gct ttt cac gcc acg cgt ata aac gag ttt tca gtc   1584
6126 Arg Leu Leu His Ala Phe His Ala Thr Arg Ile Asn Glu Phe Ser Val
6127             515                 520                 525
6129 ata aat tgt acc agg ctg gca tgg aag caa gta acc gcg ctg atg ccg   1632
6130 Ile Asn Cys Thr Arg Leu Ala Trp Lys Gln Val Thr Ala Leu Met Pro
6131       530                 535                 540
6133 ctt acg aac atc acg tac gtc ata agc tcc gtg cgc cct gat cac gct   1680
6134 Leu Thr Asn Ile Thr Tyr Val Ile Ser Ser Val Arg Pro Asp His Ala
6135 545.                550                 555                 560
6137 cgc gtt tac gag gtt tcg gag gtg ttc ctt aac agc gcg atg ttt gtc   1728
6138 Arg Val Tyr Glu Val Ser Glu Val Phe Leu Asn Ser Ala Met Phe Val
6139             565                 570                 575
6141 tcg gcc gtt tat cca aat tgt tct cat ttt aca ccg ccc ggt acc gcc   1776
6142 Ser Ala Val Tyr Pro Asn Cys Ser His Phe Thr Pro Pro Gly Thr Ala
6143             580                 585                 590
6145 cta cac att ccg ata ttg tat aac ttt tcc gcc ccg agg ata gga tgt   1824
6146 Leu His Ile Pro Ile Leu Tyr Asn Phe Ser Ala Pro Arg Ile Gly Cys
6147             595                 600                 605
6149 ccg ctg tgt gat tcg att gtt ttg agc tat gat gag aac cag gga cta   1872
6150 Pro Leu Cys Asp Ser Ile Val Leu Ser Tyr Asp Glu Asn Gln Gly Leu
6151       610                 615                 620
6153 cag acc atg atg tac gtg tca aac ccc aca gtt caa gcc aac ctg ttt   1920
6154 Gln Thr Met Met Tyr Val Ser Asn Pro Thr Val Gln Ala Asn Leu Phe
6155 625                 630                 635                 640
6157 tcc ccg tat tct cct ttc ttt gac aac gat aat ttt cat atc cat tat   1968
6158 Ser Pro Tyr Ser Pro Phe Phe Asp Asn Asp Asn Phe His Ile His Tyr
6159             645                 650                 655
6161 ttg tgg tta atg aac aac ggt acc gtt gtg gaa att cgg gga ttg tac   2016
6162 Leu Trp Leu Met Asn Asn Gly Thr Val Val Glu Ile Arg Gly Leu Tyr
6163             660                 665                 670
6165 aga aga cac gca ctc agt gct att gca tta gta ttt gct ttt att gga   2064
6166 Arg Arg His Ala Leu Ser Ala Ile Ala Leu Val Phe Ala Phe Ile Gly
6167             675                 680                 685
6169 aca atg tct gct ctg tat ttt ctg ttt aag ctg ttt tcc atc ctg gcc   2112
6170 Thr Met Ser Ala Leu Tyr Phe Leu Phe Lys Leu Phe Ser Ile Leu Ala
6171       690                 695                 700
6173 taa                                                               2115
6175 705
7909 <210> SEQ ID NO: 58
7910 <211> LENGTH: 1395
7911 <212> TYPE: DNA
7912 <213> ORGANISM: Macaca mulatta rhadinovirus 17577
7914 <220> FEATURE:
7915 <221> NAME/KEY: CDS
7916 <222> LOCATION: (1)..(1395)
7918 <400> SEQUENCE: 58
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7921   1             5                  10                  15
7923 ggg ttg ttt cac gtg ata ctt ccg cga ggg ttt atc ctc gcg aac aat    96
7924 Gly Leu Phe His Val Ile Leu Pro Arg Gly Phe Ile Leu Ala Asn Asn
7925          20                  25                  30
7927 att acg tgc ggt gaa cgg cag cgg ttt ttt gca cac act tgg ttc gct   144
7928 Ile Thr Cys Gly Glu Arg Gln Arg Phe Phe Ala His Thr Trp Phe Ala
7929          35                  40                  45
7931 gca tct gga cgc acg tct aag act tta tac gtg tgg gga cgg gta ttt   192
7932 Ala Ser Gly Arg Thr Ser Lys Thr Leu Tyr Val Trp Gly Arg Val Phe
7933       50                  55                  60
7935 caa aac acc gac ccg ggc cgc ggg gac ggt ccg tcc ggg ccg tgg tcc   240
7936 Gln Asn Thr Asp Pro Gly Arg Gly Asp Gly Pro Ser Gly Pro Trp Ser
7937    65                  70                  75                  80
7939 gga ctg gcg att agt ctg cct ctg ttt acc aca aat gga aaa ttt cat   288
7940 Gly Leu Ala Ile Ser Leu Pro Leu Phe Thr Thr Asn Gly Lys Phe His
7941          85                  90                  95
7943 ccg ttt gat gta gtt ata ctc aag gcc gat acg cct gac tct gga agc   336
7944 Pro Phe Asp Val Val Ile Leu Lys Ala Asp Thr Pro Asp Ser Gly Ser
7945          100                 105                 110
7947 tcg tgg acc gtg aag ttc ttg tat atg tca tta att gcg gct tac aga   384
7948 Ser Trp Thr Val Lys Phe Leu Tyr Met Ser Leu Ile Ala Ala Tyr Arg
7949          115                 120                 125
7951 aac gca atg cga ggt tta aaa gat aaa gtt tcg caa tgt acc gat gcc   432
7952 Asn Ala Met Arg Gly Leu Lys Asp Lys Val Ser Gln Cys Thr Asp Ala
7953       130                 135                 140
7955 gcc gtt gac ggt gag gtt cat cct cta acc gtc tta aaa gaa gcg ttg   480
7956 Ala Val Asp Gly Glu Val His Pro Leu Thr Val Leu Lys Glu Ala Leu
7957 145                 150                 155                 160
7959 gta tca ccg gac act gct acg cga ccc gtg tcc gcg tgc aac cct cta   528
7960 Val Ser Pro Asp Thr Ala Thr Arg Pro Val Ser Ala Cys Asn Pro Leu
7961          165                 170                 175
7963 cag atg ttg acc gga ctc tta cag tct agg gta cgg gac gac tac gtg   576
7964 Gln Met Leu Thr Gly Leu Leu Gln Ser Arg Val Arg Asp Asp Tyr Val
7965          180                 185                 190
7967 aca cac cac cgt gcg ctc gaa cgc cca ggt aat gtg agg gga caa gta   624
7968 Thr His His Arg Ala Leu Glu Arg Pro Gly Asn Val Arg Gly Gln Val
7969          195                 200                 205
7971 atc gcc ccg acg cgc acc gag atg cca aac gga tcg cca agt cgt gta   672
7972 Ile Ala Pro Thr Arg Thr Glu Met Pro Asn Gly Ser Pro Ser Arg Val
7973    210                 215                 220
7975 agg ctt gga ttc cgc cct ccc aaa caa gcc aac tat cca aag acg tgg   720
7976 Arg Leu Gly Phe Arg Pro Pro Lys Gln Ala Asn Tyr Pro Lys Thr Trp
7977 225                 230                 235                 240
7979 gcg cag gcg cgt cac gtt ttc tcg tct cgc gca tat tac gtg tgc gta   768
7980 Ala Gln Ala Arg His Val Phe Ser Ser Arg Ala Tyr Tyr Val Cys Val
7981                 245                 250                 255
7983 tat gat aac gaa gaa cta gat acc aag tgg cag cgg caa gat ccg cgg   816
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7984 Tyr Asp Asn Glu Glu Leu Asp Thr Lys Trp Gln Arg Gln Asp Pro Arg
7985             260                 265                 270
7987 ccg ttg ccg cta gat tgg tcc gat ccg gtc gcg tac ctg tta gag ggc   864
7988 Pro Leu Pro Leu Asp Trp Ser Asp Pro Val Ala Tyr Leu Leu Glu Gly
7989             275                 280                 285
7991 gat ttg ttt tta gga gcc aag cag aat gcg ttt gtc gat tct ata gaa   912
7992 Asp Leu Phe Leu·Gly Ala Lys Gln Asn Ala Phe Val Asp Ser Ile Glu
7993      290                 295                 300
7995 aag acg tgc agg tgt cag aac tat acc att aag caa·ttt ttt ccg gtt   960
7996 Lys Thr Cys Arg Cys Gln Asn Tyr Thr Ile Lys Gln Phe Phe·Pro Val
7997 305                 310                 315                 320
7999 ttg ata aat agg gac aac gaa aca gtc gac tta att aag gag cat ttt   1008
8000 Leu Ile Asn Arg Asp Asn Glu Thr Val Asp Leu Ile Lys Glu His Phe
8001             325                 330                 335
8003 ata gag gcg tgc ttc gtg att aga aac cag gtg tca gag agg agc gct   1056
8004 Ile Glu Ala Cys Phe Val Ile Arg Asn Gln Val Ser Glu Arg Ser Ala
8005             340                 345                 350
8007 tgg gta aag gcg gcg ctg ttt cgc aac gat agt aac acg tat tgg aag   1104
8008 Trp Val Lys Ala Ala Leu Phe Arg Asn Asp Ser Asn Thr Tyr Trp Lys
8009             355                 360                 365
8011 gat gtt ttg gga tta tgg gag cat ggg cct cat aag ctg ggt acg gct   1152
8012 Asp Val Leu Gly Leu Trp Glu His Gly Pro His Lys Leu Gly Thr Ala
8013      370                 375                 380
8015 ata aaa cta cca aca tcg gaa cct tgc aat gcc gac gta aac tgg agc   1200
8016 Ile Lys Leu Pro Thr Ser Glu Pro Cys Asn Ala Asp Val Asn Trp Ser
8017 385                 390                 395                 400
8019 tgg ctc ctg tgt gac gag gat ata act cgg tca att agc ggg cag tct   1248
8020 Trp Leu Leu Cys Asp Glu Asp Ile Thr Arg Ser Ile Ser Gly Gln Ser
8021             405                 410                 415
8023 act gtt tgc tta gtt gtc tcg cct acc ctg acc gcc tgg ctg gtg ctc   1296
8024 Thr Val Cys Leu Val Val Ser Pro Thr Leu Thr Ala Trp Leu Val Leu
8025             420                 425                 430
8027 ccg ggg ggc ttt gtt att aaa ggc cgc tac gac cta tca agc gag gat   1344
8028 Pro Gly Gly Phe Val Ile Lys Gly Arg Tyr Asp Leu Ser Ser Glu Asp
8029             435                 440                 445
8031 tta atg ttt gtg gct tcg aga tat ggc cac cca gcg tcg tca cat tct   1392
8032 Leu Met Phe Val Ala Ser Arg Tyr Gly His Pro Ala Ser Ser His Ser
8033      450                 455                 460
8035 taa                                                               1395
8037 465
16028 <210> SEQ ID NO: 148
16029 <211> LENGTH: 675
16030 <212> TYPE: DNA
16031 <213> ORGANISM: Macaca mulatta rhadinovirus 17577
16033 <220> FEATURE:
16034 <221> NAME/KEY: CDS
16035 <222> LOCATION: (1)..(675)
16037 <400> SEQUENCE: 148
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E--> (handwritten annotation)

p 52 (handwritten annotation)

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16043 Ser Tyr Leu Gly Pro Ser Gly Ile Ser Leu Asp Leu Glu Arg Cys Gln
16044              20                  25                  30
16046 gac ggg gct ccc gta tac gct aaa ggc ggg gcg gtc ccc gtg tgc acc   144
16047 Asp Gly Ala Pro Val Tyr Ala Lys Gly Gly Ala Val Pro Val Cys Thr
16048              35                  40                  45
16050 gtg cgc ctg cag cac ggc tgc gtc tat cat ctc gag ttt gtg tat aag   192
16051 Val Arg Leu Gln His Gly Cys Val Tyr His Leu Glu Phe Val Tyr Lys
16052      50                  55                  60
16054 ttt tgg ctc cac aaa cta gag aga ctg gcc tac ccg ttt gcc ccg tgt   240
16055 Phe Trp Leu His Lys Leu Glu Arg Leu Ala Tyr Pro Phe Ala Pro Cys
16056  65                  70                  75                  80
16058 ttt gta att atc aac aac ggt ttg gcc acc acg ctg aaa tgt ttt ttg   288
16059 Phe Val Ile Ile Asn Asn Gly Leu Ala Thr Thr Leu Lys Cys Phe Leu
16060                  85                  90                  95
16062 tgt aag cca cgt gac gcc gat gcc cag ttt gga aaa aac ctg cct ata   336
16063 Cys Lys Pro Arg Asp Ala Asp Ala Gln Phe Gly Lys Asn Leu Pro Ile
16064             100                 105                 110
16066 aat tcg gac gtg tat ctt gag agg aac tcg tcc gtg tcc ctg ggc cag   384
16067 Asn Ser Asp Val Tyr Leu Glu Arg Asn Ser Ser Val Ser Leu Gly Gln
16068             115                 120                 125
16070 gac gat ttt atg aaa ttt aag gca cgt ctg gtt ttc tcc gga gac cta   432
16071 Asp Asp Phe Met Lys Phe Lys Ala Arg Leu Val Phe Ser Gly Asp Leu
16072      130                 135                 140
16074 aac gtt tac agc tcc atg gtc ata tgc cgc acc tac ttt acg gag cac   480
16075 Asn Val Tyr Ser Ser Met Val Ile Cys Arg Thr Tyr Phe Thr Glu His
16076 145                 150                 155                 160
16078 cga cag gtt tta cag ttt ttg gtc gtg act cca aag agc gct aaa cgg   528
16079 Arg Gln Val Leu Gln Phe Leu Val Val Thr Pro Lys Ser Ala Lys Arg
16080                 165                 170                 175
16082 tta aaa acc ctt ctt aga acg gtt ttt gcc ctg acg ggt cac tcc gac   576
16083 Leu Lys Thr Leu Leu Arg Thr Val Phe Ala Leu Thr Gly His Ser Asp
16084             180                 185                 190
16086 ggc ctc ggt gcg ttg agg cga acg ggc tcc gtg gcc cgc cct tcg ggg   624
16087 Gly Leu Gly Ala Leu Arg Arg Thr Gly Ser Val Ala Arg Pro Ser Gly
16088             195                 200                 205
16090 tcg gag ttg aag gat att ggg cgc gga gag cgt gcg gcg atg acc aat   672
16091 Ser Glu Leu Lys Asp Ile Gly Arg Gly Glu Arg Ala Ala Met Thr Asn
16092      210                 215                 220
16094 taa                                                              675
16096 225
17824 <210> SEQ ID NO: 179
17825 <211> LENGTH: 1387
17826 <212> TYPE: DNA
17827 <213> ORGANISM: Macaca mulatta rhadinovirus 17577
17829 <400> SEQUENCE: 179
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E--> 16096

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17831 tgcgcccggg gcgagggtcc cccgcgcgcc ccccgggccc gcgcgccggg cgccgccggc 120
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17833 gccccgcgcc gcgcgccggg ccgctttcgg ttcgcggggc cggggggtccc gcggggggcc 240
17834 ggggccgccc ccgggtgccg ctccgccggg cccggccgac tcccgggagc gccccggtcc 300
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17836 gcgcgcggct cccgatgccg ggcggccgcc gccccggcatg gcggtcctcc gccggcctcc 420
17837 cctcccccac gccgccccga aaggtggtct ccgcgccgcc gggagggggg ccggggcccg 480
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17850 ggctgcctgc tggcttgctt gcttgcttgc tagtggggcc gcttgcctgc tactagggct 1260
17851 gctgtgcagc tgggagaaca gagtagggct gccggccagc tgcgtgcgag ggcgtccgag 1320
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17853 cagatct                                                        1387
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E--> 17856 (1
E--> 17859 (117)
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/831,000

DATE: 05/21/2001
TIME: 08:37:46

Input Set : A:\53683 seq listing.txt
Output Set: N:\CRF3\05212001\I831000.raw

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1172 M:254 E: No. of Bases conflict, LENGTH:Input:6800 Counted:68700 SEQ:1
M:254 Repeated in SeqNo=1
L:3738 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:4118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:4549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:5325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:6175 M:254 E: No. of Bases conflict, LENGTH:Input:705 Counted:2115 SEQ:38
L:7501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:8037 M:254 E: No. of Bases conflict, LENGTH:Input:465 Counted:1395 SEQ:58
L:8596 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:66
L:9047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:72
L:10538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:90
L:10680 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:92
L:11016 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:96
L:11337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:102
L:11403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:104
L:13405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:128
L:13729 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:132
L:13879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:134
L:14641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:140
L:15803 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:144
L:16096 M:254 E: No. of Bases conflict, LENGTH:Input:225 Counted:675 SEQ:148
L:16516 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:154
L:16622 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:156
L:17856 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:1387 SEQ:179
M:254 Repeated in SeqNo=179
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